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09/870,939	05/30/2001	Douglas A. Amorese	10010791-1	8714

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AGILENT TECHNOLOGIES, INC.  
Legal Department, DL429  
Intellectual Property Administration  
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EXAMINER

FORMAN, BETTY J

ART UNIT PAPER NUMBER

1634

DATE MAILED: 05/27/2005

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**MAILED**  
**MAY 27 2005**  
**GROUP 1600**

**BEFORE THE BOARD OF PATENT APPEALS  
AND INTERFERENCES**

Application Number: 09/870,939  
Filing Date: May 30, 2001  
Appellant(s): AMORESE ET AL.

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Bret Field  
For Appellant

**EXAMINER'S ANSWER**

This is in response to the appeal brief filed 11 January 2005.

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**(1) Real Party in Interest**

A statement identifying the real party in interest is contained in the brief.

**(2) Related Appeals and Interferences**

A statement identifying the related appeals and interferences which will directly affect or be directly affected by or have a bearing on the decision in the pending appeal is contained in the brief.

**(3) Status of Claims**

The statement of the status of the claims contained in the brief is mostly correct in that Groups II and III are correctly identified. In addition;

1) The rejection of Claims 1 and 9 under 35 U.S.C. 102(b) over Clontech is withdrawn in view of Applicant's comments on page 6 of the brief.

2) Claims 1-3, 5-14 and 38-41 are newly rejected under 35 U.S.C. 112, first paragraph, new matter.

**(4) Status of Amendments After Final**

The appellant's statement of the status of amendments after final rejection contained in the brief is correct.

**(5) Summary of Invention**

The summary of invention contained in the brief is deficient because Applicant incorrectly states that Claim 14 requires "the synthetic polynucleotides of the array are contained within the sequences of the cDNA molecules of the array". The claim is not so limited. In contrast, the claim merely requires "the sequence of a second polynucleotide is contained within a cDNA molecule." The claim language encompasses any cDNA molecule and does not limit the sequence to that of a cDNA molecule on the array as asserted. In a similar fashion, the polynucleotide sequences of Claims 11-12, 15-20 and 39-40 are not limited to the cDNAs on the array. In contrast to Applicant's assertion, the claims encompass any cDNA sequence.

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**(6) Issues**

The appellant's statement of the issues in the brief is correct.

**(7) Grouping of Claims**

The rejection of claims 1-3, 5-20 and 38-41 stand or fall together because appellant's brief does not include a statement that this grouping of claims does not stand or fall together and reasons in support thereof. See 37 CFR 1.192(c)(7).

**(8) Claims Appealed**

The copy of the appealed claims contained in the Appendix to the brief is correct.

**(9) Prior Art of Record**

6,251,601	Bao et al	06-2001
6,399,299	Bobrow et al	06-2002

**(10) Grounds of Rejection**

Claims 1-3, 5-10, 14, 38 and 41 are rejected under 35 U.S.C. 103(a) as obvious over Bao et al (U.S. Patent No. 6,251,601, filed 2 February 1999) in view of Bobrow et al (U.S. Patent No. 6,399,299, filed 29 October 1999).

Claims 11-13, 15-20 and 39-40 are rejected under 35 U.S.C. 103(a) as being unpatentable over Bao et al (U.S. Patent No. 6,251,601, filed 2 February 1999) in view of CLONTECHniques (July 2000).

These rejection are set forth in a prior Office Action, mailed on 17 August 2004.

***New Grounds of Rejection***

Claims 1-3, 5-14 and 38-41 are newly rejected under 35 U.S.C. 112, first paragraph, new matter.

These new grounds for rejection are added under 37 C.F.R. § 41.39. Applicant is advised that the revised rules require that when an examiner's answer contains a new ground of rejection, appellant must, **within two months**, either:

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1. request that prosecution be reopened by filing a § 1.111 reply; or
2. requires that the appeal be maintained by filing a reply brief, to avoid *sua sponte* dismissal of the appeal as to the claims subject to the new ground of rejection.

Claims 1-3, 5-14 and 38-41 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

In papers filed 3 June 2004, the recitation "independent of said first set of features" was added to the Independent Claims 1 and 41 (from which claims 2-3, 5-14 and 38-40 depend). Appellant pointed to page 4, lines 13-19 for support of the newly added language. For convenience, the passage is provided below:

the present invention then provides in one aspect an array of biopolymers (for example, polynucleotides such as DNA). Such an array may have a first set of multiple features each of which has first polynucleotide molecules of at least 400 nucleotides in length (for example, at least 500, 1000, or 1500 nucleotides in length). The array also may have a second set of features each of which has second polynucleotide molecules of no more than 100 nucleotides in length (for example, no more than 80, 70, or 60 nucleotides in length).

The cited passage and specification in its entirety do not teach or describe the claimed "independent" relationship of the feature sets. The passage and specification merely describe the features. The added language encompasses spatial, structural and compositional (e.g. sequence) independence. However, the specification does not teach or describe any of these independent relationships. Therefore, the specification fails to define or provide any disclosure to support such claim recitation.

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**(11) Response to Argument**

Appellant asserts that the cited art does not teach an array comprising both cDNA and synthetic oligonucleotides of the claimed length and the combination suggested by the Office would render Bao's array unsatisfactory for its intended purpose.

Appellant acknowledges that the array of Bao et al comprises target elements of greater than 400bp and less than 100bp (page 10, last paragraph of the brief). Appellant further illustrates the array of Bao et al comprising target elements that are spatially independent and comprising the claimed sequences of greater than 400bp and less than 100bp (Case 1, page 10). Appellant's comments are noted and based on Appellant's interpretation, distinguishing features of Bao et al are not apparent therein. The illustrated array (Case 1) comprises sequences greater than 400bp and sequences less than 100bp and illustrates the differing sequences as spatially separate. The instant claims are drawn to an array comprising features comprising single stranded cDNA of greater than 400bp and features comprising polynucleotides of less than 100bp. The only difference between the instant claims the reference is Appellant's assertion that cDNAs are patentably distinct from other nucleic acid sequences.

Appellant asserts that the claimed cDNAs differ from the genomic fragments on the array of Bao because the genomic fragments contain intron sequences and thus are distinguishable from the claimed cDNAs not containing introns.

Appellant's assertion of a difference between genomic fragments and cDNA is noted. However, Appellant has not defined how intron-containing genomic sequences are "distinguishable from cDNAs". Genomic sequences, intron sequences, exon sequences and cDNA sequences all have the same components i.e. nucleotides (A, T, C, G) aligned in various combinations and lengths. While all types of nucleic acid sequence (genomic, intron, exon, cDNA) vary in length and arrangement of nucleotides, the content is the same i.e. nucleotides. Because genomic, intron, exon and cDNA sequences are not distinguishable by their length or

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content, it is unclear how, absent some unclaimed defining step, the genomic sequences of Bao et al are distinguishable over cDNAs as asserted.

Appellant states (page 11, third full paragraph) that the examiner acknowledges that Bao et al do not specifically teach cDNAs and synthetic probes on the array. The statement is acknowledged, however it is further noted that the combination of Bao and Bobrow clearly teach the claimed array of cDNAs and synthetic probes and it is the combined teaching upon which the rejection is made.

As Appellant acknowledges, the Bobrow reference was cited by the office for their teaching that combination of cDNAs and oligonucleotides on an array was known in the art. Appellant asserts that Bobrow does not teach the claimed combination of cDNAs and oligonucleotides. The argument has been considered but is not found persuasive because Bobrow teaches the combinations of differing types of nucleic acids (Column 1, lines 50-55, Column 3, lines 30-35 and Claim 1). However, given Appellant's interpretation of Bao et al, the Bobrow reference is not essential to the elements at issue. That issue being a distinguishing of cDNA sequences over genomic sequences.

Appellant acknowledges and illustrates that Bao et al teach genomic fragments and oligonucleotides at independent features on an array (page 10). Appellant, however, asserts that the genomic features of Bao (illustrated as "Case 1) contain intron sequences and are therefore different from the claimed cDNA. Appellant's arguments are noted. However, Bao specifically teach their genomic fragment contain exon sequences which code for all or part of the expressed sequence (Column 6, lines 56-58). Therefore, the genomic sequences of Bao contain expressed sequences. The instant claims are drawn to cDNAs and contain the open claim language "comprising". The claims are not limited to exclude introns, non-coding sequences, or complementary strands. IN view of the open claim language "comprising" and in view of the teaching of Bao wherein their genomic fragments contain expressed sequences, it

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is unclear to the examiner how the broadly claimed sequences are distinguishable over those of Bao.

Appellant asserts that the array of Bao et al is intended for simultaneous analysis of gene expression and chromosomal abnormalities and if modified to contain cDNAs and oligonucleotides as claimed, the modified array would be unsatisfactory for the purpose of Bao. The arguments has been considered but is not found persuasive because as discussed above and acknowledged by Appellant, Bao et al clearly teach the combination of genomic fragments and oligonucleotides of the claimed lengths. Because Bao et al teach the structural elements of the claimed array, arguments regarding an intended use are not relevant to the instant product claims.

Appellant argues that Bao does not teach that a sequence of a second polynucleotide is contained within a cDNA molecule sequence present in different elements as claimed in Claim 14 and 41. The argument has been considered but is not found persuasive because the argument is not commensurate in scope with the claim 14. The claim requires "the sequence of a second polynucleotide is contained within a cDNA. The claim is not limited to the second polynucleotide or the cDNA of Claim 1. Furthermore, the claim is not limited to the second polynucleotide of Claim 1 be within the cDNA of Claim 1. In contrast, the claim merely requires a second polynucleotide sequence be within a cDNA. Hence, the synthetic polynucleotides comprising partial cDNAs (Column 8, lines 39-42) of Bao et al are within a cDNA as claimed. Regarding Claim 41, Bao et al specifically teach the oligomer DNA targets measure expression (Column 3, lines 64-Column 4, line 1) and the genomic fragments measure chromosomal region having the same expressed region (Column 6, lines 63-67). From this teaching it is clear that a sequence of the oligomer DNAs is within genomic fragments.

Regarding the rejections of Bao et al in view of CLONTECHniques, Appellant cites the arguments discussed above and further asserts that CLONTECHniques does not cure the




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deficiency of Bao. The argument has been considered but is not found persuasive for the reasons stated above regarding Bao.

For the above reasons, it is believed that the rejections should be sustained.


Respectfully submitted,

BJ Forman  
Primary Examiner  
Art Unit 1634


  
BJ Forman  
May 25, 2005

  
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